

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/747,702
Source: IFND
Date Processed by STIC: 10-07-2005

ENTERED



IFWO

RAW SEQUENCE LISTING

DATE: 10/07/2005

PATENT APPLICATION: US/10/747,702

TIME: 12:54:20

Input Set : N:\Crif3\RULE60\10747702.raw.txt

Output Set: N:\CRF4\10062005\J747702.raw

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1 <110> APPLICANT: Ahmad, Sultan
2   Banville, Denis
3   Fortin, Yves
4   Lembo, Paola
5   O'Donnell, Dajan
6   Shi-Hsiang, Shen
7 <120> TITLE OF INVENTION: G Protein-Coupled Receptors from the Rat and Human
8 <130> FILE REFERENCE: 81823/268117
9 <140> CURRENT APPLICATION NUMBER: US/10/747,702
C--> 10 <141> CURRENT FILING DATE: 2003-12-30
11 <150> PRIOR APPLICATION NUMBER: Prio APPLICATION NUMBER: US/09/254,227
12 <151> PRIOR FILING DATE: 1999-03-03
13 <160> NUMBER OF SEQ ID NOS: 22
14 <170> SOFTWARE: PatentIn version 3.0
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 337
18 <212> TYPE: PRT
19 <213> ORGANISM: rat
20 <400> SEQUENCE: 1
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24           20           25           30
25   Gly His Pro Ser Cys Arg Pro Ile Leu Thr Leu Ser Phe Leu Val Pro
26           35           40           45
27   Ile Ile Thr Leu Leu Gly Leu Ala Gly Asn Thr Ile Val Leu Trp Leu
28           50           55           60
29   Leu Gly Phe Arg Met Arg Arg Lys Ala Ile Ser Val Tyr Val Leu Asn
30           65           70           75           80
31   Leu Ser Leu Ala Asp Ser Phe Phe Leu Cys Cys His Phe Ile Asp Ser
32           85           90           95
33   Leu Met Arg Ile Met Asn Phe Tyr Gly Ile Tyr Ala His Lys Leu Ser
34           100          105          110
35   Lys Glu Ile Leu Gly Asn Val Ala Phe Ile Pro Tyr Ile Ser Gly Leu
36           115          120          125
37   Ser Ile Leu Ser Ala Ile Ser Thr Glu Arg Cys Leu Ser Val Leu Trp
38           130          135          140
39   Pro Ile Trp Tyr His Cys His Arg Pro Arg Asn Met Ser Ala Ile Ile
40           145          150          155          160
41   Cys Val Leu Ile Trp Val Leu Ser Phe Leu Met Gly Ile Leu Asp Trp
42           165          170          175
43   Phe Phe Ser Gly Phe Leu Gly Glu Thr His His His Leu Trp Lys Asn
44           180          185          190

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45      Val Asp Phe Ile Val Thr Ala Phe Leu Ile Phe Leu Phe Met Leu Leu
46          195                      200                      205
47      Phe Gly Ser Ser Leu Ala Leu Leu Val Arg Ile Leu Cys Gly Ser Arg
48          210                      215                      220
49      Arg Lys Pro Leu Ser Arg Leu Tyr Val Thr Ile Ser Leu Thr Val Met
50          225                      230                      235                      240
51      Val Tyr Leu Ile Cys Gly Leu Pro Leu Gly Leu Tyr Leu Phe Leu Leu
52          245                      250                      255
53      Tyr Trp Phe Gly Ile His Leu His Tyr Pro Phe Cys His Ile Tyr Gln
54          260                      265                      270
55      Val Thr Val Leu Leu Ser Cys Val Asn Ser Ser Ala Asn Pro Ile Ile
56          275                      280                      285
57      Tyr Phe Leu Val Gly Ser Phe Arg His Arg Lys Lys His Arg Ser Leu
58          290                      295                      300
59      Lys Met Val Leu Lys Arg Ala Leu Glu Glu Thr Pro Glu Glu Asp Glu
60          305                      310                      315                      320
61      Tyr Thr Asp Ser His Val Gln Lys Pro Thr Glu Ile Ser Glu Arg Arg
62          325                      330                      335
63      Cys
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65 <211> LENGTH: 1011
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72      ctcaccctgt ccttcctggg ccccatcatc accctgcttg gattggcagg aaacaccatt      180
73      gtactctggc tcttgggatt ccgcatgcgc aggaaagcca tctcagtcta cgtcctcaac      240
74      ctgtctctgg cagactcctt ctctctctgc tgccatttta ttgactctct gatgcggatc      300
75      atgaacttct atggcatcta tgcccataaa ttaagcaaag aaatcttagg caatgtagca      360
76      ttcatccctt atatctcagg cctgagcatc ctcagtgcta tcagcacgga gcgctgcctg      420
77      tctgtattgt ggccaatctg gtaccactgc caccgcccga gaaacatgtc agctattata      480
78      tgtgttctaa tctgggttct gtcccttctc atgggcatcc ttgactgggt tttctcagga      540
79      ttccctgggtg agactcacca tcatttgggt aaaaatgttg actttattgt aactgcattt      600
80      ctgatttttt tatttatgct tctctttggg tccagtctgg cgctactggg gaggatcctc      660
81      tgtggttcca gacggaaaacc actgtccagg ctgtacgtta caatctctct cacagtgatg      720
82      gtctacctca tctgcggcct gcctctcggg ctttacttgt tcctgctata ttggtttggg      780
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84      aacagctctg ccaaccccat catttacttc cttgtagggt cctttaggca ccgtaaaaag      900
85      catcggtccc tcaaaatggg tcttaaaagg gctctggagg agactcctga ggaggatgaa      960
86      tatacagaca gccatgttca gaaaccact gagatctcag aaaggagatg t      1011
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88 <211> LENGTH: 322
89 <212> TYPE: PRT
90 <213> ORGANISM: Homo sapiens
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93          1                      5                      10                      15
94      Gly Arg Glu Glu Thr Pro Cys Tyr Asn Gln Thr Leu Ser Phe Thr Gly

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96          20          25          30
97  Leu Thr Cys Ile Ile Ser Leu Val Ala Leu Thr Gly Asn Ala Val Val
98          35          40          45
99  Leu Trp Leu Leu Gly Cys Arg Met Arg Arg Asn Ala Val Ser Ile Tyr
100         50          55          60
101  Ile Leu Asn Leu Val Ala Ala Asn Phe Leu Phe Leu Ser Gly His Ile
102         65          70          75          80
103  Ile Phe Ser Pro Leu Pro Leu Ile Asn Ile Arg His Pro Ile Ser Lys
104          85          90          95
105  Ile Leu Ser Pro Val Met Thr Phe Pro Tyr Phe Ile Gly Leu Ser Met
106          100         105         110
107  Leu Ser Ala Ile Ser Thr Glu Arg Cys Leu Ser Ile Leu Trp Pro Ile
108          115         120         125
109  Trp Tyr His Cys Arg Arg Pro Arg Tyr Leu Ser Ser Val Met Cys Val
110          130         135         140
111  Leu Leu Trp Ala Leu Ser Leu Leu Arg Ser Ile Leu Glu Trp Met Phe
112          145         150         155         160
113  Cys Asp Phe Leu Phe Ser Gly Ala Asn Ser Val Trp Cys Glu Thr Ser
114          165         170         175
115  Asp Phe Ile Thr Ile Ala Trp Leu Val Phe Leu Cys Val Val Leu Cys
116          180         185         190
117  Gly Ser Ser Leu Val Leu Leu Val Arg Ile Leu Cys Gly Ser Arg Lys
118          195         200         205
119  Met Pro Leu Thr Arg Leu Tyr Val Thr Ile Leu Leu Thr Val Leu Val
120          210         215         220
121  Phe Leu Leu Cys Gly Leu Pro Phe Gly Ile Gln Trp Ala Leu Phe Ser
122          225         230         235         240
123  Arg Ile His Leu Asp Trp Lys Val Leu Phe Cys His Val His Leu Val
124          245         250         255
125  Ser Ile Phe Leu Ser Ala Leu Asn Ser Ser Ala Asn Pro Ile Ile Tyr
126          260         265         270
127  Phe Phe Val Gly Ser Phe Arg Gln Arg Gln Asn Arg Gln Asn Leu Lys
128          275         280         285
129  Leu Val Leu Gln Arg Ala Leu Gln Asp Thr Pro Glu Val Asp Glu Gly
130          290         295         300
131  Gly Gly Trp Leu Pro Gln Glu Thr Leu Glu Leu Ser Gly Ser Lys Leu
132          305         310         315         320
133  Glu Gln
135 <210> SEQ ID NO: 4
136 <211> LENGTH: 969
137 <212> TYPE: DNA
138 <213> ORGANISM: Homo sapiens
139 <400> SEQUENCE: 4
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142  gcgctgacag gaaacgcggt tgtgctctgg ctccctgggt gccgcatgcg caggaacgct 180
143  gtctccatct acatcctcaa cctggctcgc gccaaattcc tcttccttag cggccacatt 240
144  atattttcgc cgttaccctt catcaatatc cgccatccca tctccaaaat cctcagtcct 300
145  gtgatgacct ttccctactt tataggccta agcatgctga gcgccatcag caccgagcgc 360

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146      tgcctgtcca tctgtggcc catctggtac cactgccgcc gcccagata cctgtcatcg      420
147      gtcattgtgtg tctgtctctg ggccctgtcc ctgctgcgga gtatcctgga gtggatgttc      480
148      tgtgacttcc tgttttagtg tgctaattct gtttggtgtg aaacgtcaga ttccattaca      540
149      atcgcggtggc tggttttttt atgtgtggtt ctctgtgggt ccagcctggt cctgtctggtc      600
150      aggattctct gtggatcccg gaagatgccg ctgaccaggc tgtacgtgac catcctctctc      660
151      acagtgtctgg tcttctctct ctgtggcctg ccttttgga ttcagtgggc cctgttttcc      720
152      aggatccacc tggattggaa agtcttattt tgtcatgtgc atctagtttc cattttcctg      780
153      tccgctctta acagcagtgc caaccccatc atttacttct tcgtgggctc ctttaggcag      840
154      cgtcaaaata ggcaaaacct gaagctgggt ctccaaaggg ctctgcagga cagcctgag      900
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165      Gly Arg Glu Glu Thr Pro Cys Tyr Lys Gln Thr Leu Ser Phe Thr Gly
166      20          25          30
167      Leu Thr Cys Ile Val Ser Leu Val Ala Leu Thr Gly Asn Ala Val Val
168      35          40          45
169      Leu Trp Leu Leu Gly Cys Arg Met Arg Arg Asn Ala Val Ser Ile Tyr
170      50          55          60
171      Ile Leu Asn Leu Val Ala Ala Asp Phe Leu Phe Leu Ser Gly His Ile
172      65          70          75          80
173      Ile Cys Ser Pro Leu Arg Leu Ile Asn Ile Ser His Pro Ile Ser Lys
174      85          90          95
175      Ile Leu Ser Pro Val Met Thr Phe Pro Tyr Phe Ile Gly Leu Ser Met
176      100         105         110
177      Leu Asn Ala Ile Ser Thr Glu Arg Cys Leu Ser Ile Leu Trp Pro Ile
178      115         120         125
179      Trp Tyr His Cys Arg Arg Pro Arg Tyr Leu Ser Ser Val Met Cys Val
180      130         135         140
181      Leu Leu Trp Ala Pro Ser Leu Leu Arg Ser Ile Leu Glu Trp Met Phe
182      145         150         155         160
183      Cys Asp Phe Leu Phe Ser Gly Ala Asp Ser Val Arg Cys Glu Thr Ser
184      165         170         175
185      Asp Phe Ile Thr Ile Ala Trp Leu Val Phe Leu Arg Val Val Leu Cys
186      180         185         190
187      Gly Ser Ser Leu Val Leu Leu Val Arg Ile Leu Cys Gly Ser Arg Lys
188      195         200         205
189      Met Pro Leu Thr Arg Leu Tyr Val Thr Ile Leu Leu Thr Val Leu Val
190      210         215         220
191      Phe Leu Leu Cys Gly Leu Pro Phe Gly Ile Gln Trp Ala Leu Phe Ser
192      225         230         235         240
193      Arg Ile His Leu Asp Trp Lys Val Leu Phe Cys His Val His Leu Val
194      245         250         255
195      Ser Ile Phe Leu Ser Ala Leu Asn Ser Ser Ala Asn Pro Ile Ile Tyr

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Output Set: N:\CRF4\10062005\J747702.raw

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196          260          265          270
197      Phe Phe Met Gly Ser Phe Arg Gln Leu Gln Asn Arg Lys Thr Leu Lys
198          275          280          285
199      Leu Val Leu Gln Arg Asp Leu Gln Asp Thr Pro Glu Val Asp Glu Gly
200          290          295          300
201      Gly Trp Trp Leu Pro Gln Glu Thr Leu Glu Leu Ser Gly Ser Lys Leu
202      305          310          315          320
203      Glu Ile
205 <210> SEQ ID NO: 6
206 <211> LENGTH: 969
207 <212> TYPE: DNA
208 <213> ORGANISM: Homo sapiens
209 <400> SEQUENCE: 6
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212      gcgctgacag gaaacgcggt tgtgctctgg ctcttgggct gccgcatgcg caggaacgct      180
213      gtctccatct acatcctcaa cctggctcgc gccgacttcc tcttccttag cggccacatt      240
214      atatgttcgc cgttacgcct catcaatc agccatccca tctccaaaat ctcagtcct      300
215      gtgatgacct ttccctactt tataggccta agcatgctga acgccatcag caccgagcgc      360
216      tgctgtgcca tctgtgggcc catctgggtac cactgccgcc gccccagata cctgtcatcg      420
217      gtcattgtgtg tctgtctctg ggccccgtcc ctgctgcgga gtatcctgga gtggatgttc      480
218      tgtgacttcc tgtttagtgg tgcctgattc gttcgggtgtg aaacgtcaga ttctattaca      540
219      atcgcgtggc tggttttttt acgtgtgggt ctctgtgggt ccagcctggt cctgctgggtc      600
220      aggattctct gtggatcccc gaagatgccg ctgaccaggc tgtacgtgac catcctctct      660
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223      tccgctctta acagcagtgc caaccccatc atttacttct tcatgggctc ctttaggcag      840
224      cttcaaaaca ggaagaccct caagctgggt ctccagaggg atctgcagga caccgctgag      900
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226      gagatctga      969
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229 <211> LENGTH: 322
230 <212> TYPE: PRT
231 <213> ORGANISM: Homo sapiens
232 <400> SEQUENCE: 7
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234      1          5          10          15
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236          20          25          30
237      Leu Thr Cys Ile Val Ser Leu Val Gly Leu Thr Gly Asn Ala Val Val
238          35          40          45
239      Leu Trp Leu Leu Gly Cys Arg Met Arg Arg Asn Ala Phe Ser Ile Tyr
240          50          55          60
241      Ile Leu Asn Leu Ala Ala Asp Phe Leu Phe Leu Ser Gly Arg Leu
242      65          70          75          80
243      Ile Tyr Ser Leu Leu Ser Phe Ile Ser Ile Pro His Thr Ile Ser Lys
244          85          90          95
245      Ile Leu Tyr Pro Val Met Met Phe Ser Tyr Phe Ala Gly Leu Asn Phe
246          100          105          110

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RAW SEQUENCE LISTING ERROR SUMMARY

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Input Set : N:\Crf3\RULE60\10747702.raw.txt

Output Set: N:\CRF4\10062005\J747702.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:15; N Pos. 25,28,31,34

Seq#:16; N Pos. 10,13

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10747702.raw.txt

Output Set: N:\CRF4\10062005\J747702.raw

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:517 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0

L:528 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0